* *
Reviewer Comments:
<210> 2
<211> 1209
<212> DNA
<213> Unknown

<220>
<223> environmental sample

<221> misc_feature
<222> 734
<223> n = A,T,C or G

<400> 2
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ggagcagcct tcgcctcgcg ggatgtagtc ctggtgacgg tgaattaccg tcttggccat
120
ctcggctttt tcgcccatcc ggcgctggat gaagaaaatc cagacggccc ggttcataat
180
ttcgcgcttt tagaccaaat tgctgccctg aaatgggtgc aggaaaatat cgctgctttc
240
ggcggcgacg cggggaatgt cacgctgttt ggcgagtctg ccggggcgcg tagcgtgctt
300
tcgctgctgg cgtcgccgct ggcgaaaaac cttttccaca aggtattat acaaagcgcc
360
tacacgttgc cggatgtcga caggaagaaa gccctgaaac gtggcgtagc gctggccggt
420
cattacgggc tgcaaaatgc cacagcggat gaactccgcg ctctgcctgc ggatgggctg
480

tgggcgcttg aagggccgct taacattggt ccaacgccaa tctccggcga cgtcgtgctg
540

cctgagccga tgctggatat attcttcgcc gggcgtcagc accgcatgcc cttgatggtc
600

gggagcaaca gcgacgaggc aagcgtgctg agctacttcg catcgatcc tgccgggcag
660

gtcgaactgc tgcgccgggg agcggcgttt ccggactggg ggcttatcaa actgctgtat
720

tcccggagtg aaangggat gcccgaactc gggcgacagg tgtgccgcga tatggctttt
780

nccncgctgg gttttgttgt gatgcaggcc cagcagcggg tcaatcagcc ctgctggcgc
840

The above <222> response only indicates one "n" location (734); however,
n's are also located at 781 and 784: please explain them.

(from Sequence 3)
<221> VARIANT
<222> 245, 260, 261
<223> Xaa = Any Amino Acid

<400> 3
Met Val Trp Leu His Gly Gly Gly Tyr Thr Ile Gly Ala Gly Ser Leu
 1   5   10   15

Pro Pro Tyr Asp Gly Ala Ala Phe Ala Ser Arg Asp Val Val Leu Val
            20   25   30

Thr Val Asn Tyr Arg Leu Gly His Leu Gly Phe Phe Ala His Pro Ala
            35   40   45

Leu Asp Glu Glu Asn Pro Asp Gly Pro Val His Asn Phe Ala Leu Leu
        50   55   60

Asp Gln Ile Ala Ala Leu Lys Trp Val Gln Glu Asn Ile Ala Ala Phe
65   70   75   80

Gly Gly Asp Ala Gly Asn Val Thr Leu Phe Gly Glu Ser Ala Gly Ala
                85   90   95

Arg Ser Val Leu Ser Leu Leu Ala Ser Pro Leu Ala Lys Asn Leu Phe
                100   105   110

His Lys Gly Ile Ile Gln Ser Ala Tyr Thr Leu Pro Asp Val Asp Arg
                115   120   125

Lys Lys Ala Leu Lys Arg Gly Val Ala Leu Ala Gly His Tyr Gly Leu
        130   135   140

Gln Asn Ala Thr Ala Asp Glu Leu Arg Ala Leu Pro Ala Asp Gly Leu

```
     145                         150                         155                         160
Trp Ala Leu Glu Gly Pro Leu Asn Ile Gly Pro Thr Pro Ile Ser Gly
                    165                         170                         175
Asp Val Val Leu Pro Glu Pro Met Leu Asp Ile Phe Phe Ala Gly Arg
                    180                         185                         190
Gln His Arg Met Pro Leu Met Val Gly Ser Asn Ser Asp Glu Ala Ser
                    195                         200                         205
Val Leu Ser Tyr Phe Gly Ile Asp Pro Ala Gly Gln Val Glu Leu Leu
     210                         215                         220
Arg Arg Gly Ala Ala Phe Pro Asp Trp Gly Leu Ile Lys Leu Leu Tyr
225                         230                         235                         240
Ser Arg Ser Glu Xaa Gly Met Pro Glu Leu Gly Arg Gln Val Cys Arg
                    245                         250                         255
Asp Met Ala Phe Xaa Xaa Leu Gly Phe Val Val Met Gln Ala Gln Gln
                    260                         265                         270
```

The above <222> response is incorrect: while Xaa is located at 245,
"Phe" is located at 260 (not Xaa). Xaa's are located at 261 and 262.

* *

Application No: 10555587   Version No: 1.0

Input Set:

Output Set:

        Started: 2007-08-01 10:04:38.617
       Finished: 2007-08-01 10:04:39.579
        Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 962 ms
 Total Warnings: 3
   Total Errors: 8
No. of SeqIDs Defined: 3
Actual SeqID Count: 3

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
E 342	'n' position not defined found at POS: 1926 SEQID(1)
E 342	'n' position not defined found at POS: 1973 SEQID(1)
E 342	'n' position not defined found at POS: 1976 SEQID(1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
E 342	'n' position not defined found at POS: 781 SEQID(2)
E 342	'n' position not defined found at POS: 784 SEQID(2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
E 341	'Xaa' position not defined SEQID (3) POS (245)
E 341	'Xaa' position not defined SEQID (3) POS (261)
E 341	'Xaa' position not defined SEQID (3) POS (262)

<110> Genencor International, Inc.
        Jones, Brian E.
        Grant, William D.
        Heaphy, Shaun
        Rees, Helen C.
        Grant, Susan

<120> Novel Lipolytic Enzyme LIP1

<130> GC801-2-PCT

<140> 10555587
<141> 2007-08-01

<150>   PCT/US04/014752
<151>   2004-05-12

<150> US 60/469,931
<151> 2003-05-12

<160> 3

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 4313
<212> DNA
<213> Unknown

<220>
<223> environmental sample

<221> misc_feature
<222> 1926, 1973, 1976
<223> n = A,T,C or G

<400> 1
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atgatgagca ccggctgatc gccgatgtag tctgcttccg tggctgccac attaaccacc   180
tgaccccgcg cacgctcgat atcgaccgcg tgcagtcgct gatgccggaa cgcggaatta   240
ccccaaaagc cattatcgaa gggccgccgc gccgcgagcg cccgatttta ctgcgccaga   300
ccagctttaa agcgctggaa gagcctattt tgttcgccgg tgagcatcac ggaacgcata   360
ccgcccgttt cggcgaaata gaacagcgcg gcgtagcgct gacgccgaaa ggccgggcgc   420
tgtacgacga actgctgctg gcggcgggca acggcacgga taatctcagc caccagcagc   480
atttacacga agtgttcacc gtttcccgga cagcgacgcg ctgctgcgcc gccaggggct   540
ggcctatttc cgctatcgtt tgacgcccgt tggcgaaatg caccgccact caatcaagcc   600
aggcgacgac ccgcagctgc ttatagaacg cggctggctg gtggcgcagc cggttatttta   660
tgaagatttc ctcccggtca gcgcggcggg tattttccag tcaaaccttg gcagcgacgg   720
cgggcaacgg cagcacggcc attccagccg cagcgagttt gaacaggccc ttggcgcaga   780
ggttgcagac gagttcgccc tctatcagca ggccgaggat cgcagtaaac gccgttgcgg   840
tttgctgtaa acgcgctacc ctgctggagt gtcagtaaca aggaacagca gatggaacaa   900
gttgttagcc gttgctcagg ggagactgag cggcgttctt caggggaaag ttgcggtcta   960

```
tcgcggcatc cccttttgccg ctccgccggt gggtgaactg cgctggcggg cacctcgtcc      1020
cccggcgcac tggcagggta tccgccaggc ggatacattt gcgcctgcat gctggcaaag      1080
cctcgaatac tgcaaagcgg ttggcggcgg cgatcccggc cagtttttctg aagattgcct     1140
gtatctcaat atctggaccc cggcccggcg ggatgcggag ccgctgccgg ttatggtctg       1200
gctgcacggt gggggctaca ctatcggcgc aggctcgctg ccgccctacg atggagcagc       1260
cttcgcctcg cgggatgtag tcctggtgac ggtgaattac cgtcttggcc atctcggctt       1320
tttcgcccat ccggcgctgg atgaagaaaa tccagacggc ccggttcata atttcgcgct       1380
tttagaccaa attgctgccc tgaaatgggt gcaggaaaat atcgctgctt tcggcggcga       1440
cgcggggaat gtcacgctgt ttggcgagtc tgccgggggcg cgtagcgtgc tttcgctgct      1500
ggcgtcgccg ctggcgaaaa acctttttcca caaaggtatt atacaaagcg cctacacgtt      1560
gccggatgtc gacaggaaga aagccctgaa acgtggcgta gcgctggccg gtcattacgg       1620
gctgcaaaat gccacagcgg atgaactccg cgctctgcct gcggatgggc tgtgggcgct       1680
tgaagggccg cttaacattg gtccaacgcc aatctccggc gacgtcgtgc tgcctgagcc       1740
gatgctggat atattcttcg ccgggcgtca gcaccgcatg cccttgatgg tcgggagcaa       1800
cagcgacgag gcaagcgtgc tgagctactt cggcatcgat cctgccgggc aggtcgaact      1860
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agtgccgtat gttttttgaca cgttaagtct gacgccaccc gcaagtgaat acgtcaacca      2160
aaacgatctc acgtttgccg ggcaaatttg tgactactgg acccgttttg cccgcagcgc      2220
cggtcccccac agtaaagcga taccgggccc gctaagctgg cctgcctgcg ttcgcggcaa     2280
ggaccgaacg atgcggttag gcgttcactc gcgggcgcgg ttcaaagtgg aaaaccgctt      2340
tatgcgcatg agaatgcagc tgtttaagcg ggtcatgaag catcacgtca gccttgactg      2400
agcaactcat ggcaaaatgc ttcaagcccg gcggcgtgct cgctgccggg tttaaccgcc      2460
agacggtagc ccgcaccggt ttttacactg cgatcaaacg gcctgaccag ccgcccggta      2520
cgaatatctt ctgccaccag cgtttcatcg gcgatggcga tcccaaaccc ctgaatagcg      2580
gcgctgatgg cgagatccat agtgtcaaaa tgctgatttt tactcattgc ctgccagggc      2640
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aatgtcagtc tttcccagcc gctatcttct tttggcagca ggctctggct tacaaccggc      2760
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tgtagctccg gcatgcgttg ttcaagctga atcagctttg gcaccagcca gcgcatcgcg      2940
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catgatgctc tccgttgagc tatgcatttt ttgcatggct attatgacaa caattcgatt      3300
gtcgtggcaa tcgcatccgg attgaatagt tatgcaaatc gcatattgtt caggagcggc      3360
tatggccatg caaaccccgg tgcaacatcg ttcaaaactg ccggatgtag gaaccaccat      3420
atttacggtt atcggtcagc tttccgccca acataaggcg atcaaccttt ctcaggcgc       3480
gcccaacttc ccctgtgacc cgcagcttat tgccggagtc accagggcaa tgcaggaggg      3540
gcataaccag tatgcgtcca tgaccggact tgcgtcgctg aaaaatctta ttgctgaaaa      3600
agtcgcggcg ctttacggct caacctacga tccggcggat gaagtgctgg ttaccgccag      3660
cgccagcgaa gggctgtatt ccgctatcgg cggactggta caccccggcg acgaagttat      3720
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cataacgccg cgtacccgca tgattattgt caacacgccg cataacccaa gcgggcaggt      3900
gttcagcgct catgatctcg aaatgctggc ggcgcttacc cgtaatacgg atatcgttgt      3960
cctgtctgac gaagtgtacg agcacatcgt gtttgacgga caaaagcatc acggcatggc      4020
cacgcacccg cagcttgccg agcgtagcgt tatcgtttca tcgtttggca aaaccttcca      4080
tgttaccggc tggcgcgtgg ggtactgcct ggcgcccgcc gcgttgatgg atgagatttg      4140
caaggtgcat cagttcctga tgttttcagc cgatacgcca atgcagcacg cttttgctga      4200
ttacatgagc gatccgcaaa cttatctctc gctggcgagc ctttaccagc gcaagcgtga      4260
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<210> 2
<211> 1209
<212> DNA
<213> Unknown

<220>
<223> environmental sample

<221> misc_feature
<222> 734
<223> n = A,T,C or G

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ctcggctttt tcgcccatcc ggcgctggat gaagaaaatc cagacggccc ggttcataat   180
ttcgcgcttt tagaccaaat tgctgccctg aaatgggtgc aggaaaatat cgctgctttc   240
ggcggcgacg cggggaatgt cacgctgttt ggcgagtctg ccggggcgcg tagcgtgctt   300
tcgctgctgg cgtcgccgct ggcgaaaaac cttttccaca aaggtattat acaaagcgcc   360
tacacgttgc cggatgtcga caggaagaaa gccctgaaac gtggcgtagc gctggccggt   420
cattacgggc tgcaaaatgc cacagcggat gaactccgcg ctctgcctgc ggatgggctg   480
tgggcgcttg aagggccgct aacattggt ccaacgccaa tctccggcga cgtcgtgctg   540
cctgagccga tgctggatat attcttcgcc gggcgtcagc accgcatgcc cttgatggtc   600
gggagcaaca gcgacgaggc aagcgtgctg agctacttcg gcatcgatcc tgccgggcag   660
gtcgaactgc tgcgccgggg agcggcgttt ccggactggg ggcttatcaa actgctgtat   720
tcccggagtg aaangggat gccccgaactc gggcgacagg tgtgccgcga tatggctttt   780
nccncgctgg gttttgttgt gatgcaggcc cagcagcggg tcaatcagcc ctgctggcgc   840
tactattttg attatgtggg ggaggcggaa cgtaaaatct atgccaacgg cacctggcac   900
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cgcggcaagg accgaacgat gcggttaggc gttcactcgc gggcgcggtt caaagtggaa   1140
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<210> 3
<211> 402
<212> PRT
<213> Unknown

<220>
<223> environmental sample

<221> VARIANT
<222> 245, 260, 261
<223> Xaa = Any Amino Acid

<400> 3
Met Val Trp Leu His Gly Gly Gly Tyr Thr Ile Gly Ala Gly Ser Leu
1   5   10   15
Pro Pro Tyr Asp Gly Ala Ala Phe Ala Ser Arg Asp Val Val Leu Val
            20   25   30
Thr Val Asn Tyr Arg Leu Gly His Leu Gly Phe Phe Ala His Pro Ala
        35   40   45
Leu Asp Glu Glu Asn Pro Asp Gly Pro Val His Asn Phe Ala Leu Leu
    50   55   60
Asp Gln Ile Ala Ala Leu Lys Trp Val Gln Glu Asn Ile Ala Ala Phe

```
            65                          70                          75                          80
Gly Gly Asp Ala Gly Asn Val Thr Leu Phe Gly Glu Ser Ala Gly Ala
                    85                          90                          95
Arg Ser Val Leu Ser Leu Leu Ala Ser Pro Leu Ala Lys Asn Leu Phe
                   100                         105                         110
His Lys Gly Ile Ile Gln Ser Ala Tyr Thr Leu Pro Asp Val Asp Arg
        115                         120                         125
Lys Lys Ala Leu Lys Arg Gly Val Ala Leu Ala Gly His Tyr Gly Leu
        130                         135                         140
Gln Asn Ala Thr Ala Asp Glu Leu Arg Ala Leu Pro Ala Asp Gly Leu
145                         150                         155                         160
Trp Ala Leu Glu Gly Pro Leu Asn Ile Gly Pro Thr Pro Ile Ser Gly
                   165                         170                         175
Asp Val Val Leu Pro Glu Pro Met Leu Asp Ile Phe Phe Ala Gly Arg
                   180                         185                         190
Gln His Arg Met Pro Leu Met Val Gly Ser Asn Ser Asp Glu Ala Ser
        195                         200                         205
Val Leu Ser Tyr Phe Gly Ile Asp Pro Ala Gly Gln Val Glu Leu Leu
        210                         215                         220
Arg Arg Gly Ala Ala Phe Pro Asp Trp Gly Leu Ile Lys Leu Leu Tyr
225                         230                         235                         240
Ser Arg Ser Glu Xaa Gly Met Pro Glu Leu Gly Arg Gln Val Cys Arg
                   245                         250                         255
Asp Met Ala Phe Xaa Xaa Leu Gly Phe Val Val Met Gln Ala Gln Gln
                   260                         265                         270
Arg Val Asn Gln Pro Cys Trp Arg Tyr Tyr Phe Asp Tyr Val Gly Glu
                   275                         280                         285
Ala Glu Arg Lys Ile Tyr Ala Asn Gly Thr Trp His Gly Asn Glu Val
        290                         295                         300
Pro Tyr Val Phe Asp Thr Leu Ser Leu Thr Pro Pro Ala Ser Glu Tyr
305                         310                         315                         320
Val Asn Gln Asn Asp Leu Thr Phe Ala Gly Gln Ile Cys Asp Tyr Trp
                   325                         330                         335
Thr Arg Phe Ala Arg Ser Ala Gly Pro His Ser Lys Ala Ile Pro Gly
                   340                         345                         350
Pro Leu Ser Trp Pro Ala Cys Val Arg Gly Lys Asp Arg Thr Met Arg
                   355                         360                         365
Leu Gly Val His Ser Arg Ala Arg Phe Lys Val Glu Asn Arg Phe Met
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Arg Met Arg Met Gln Leu Phe Lys Arg Val Met Lys His His Val Ser
385                         390                         395                         400
Leu Asp
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